

**Patent claims**

1. Genetically modified plant cell, characterised in that it has a reduced activity of at least one Class 3 branching enzyme in comparison with corresponding wild type plant cells that have not been genetically modified.
2. Genetically modified plant cell according to Claim 1, wherein the genetic modification consists in the introduction of at least one foreign nucleic acid molecule into the genome of the plant cell.
3. Genetically modified plant cell according to Claim 2, wherein the foreign nucleic acid molecule codes a Class 3 branching enzyme.
4. Genetically modified plant cell according to Claim 3, wherein the said foreign nucleic acid molecule is chosen from the group consisting of
  - a) Nucleic acid molecules, which code a protein with the amino acid sequence given under Seq ID No. 4;
  - b) Nucleic acid molecules, which code a protein, the amino acid sequence of which has an identity of at least 50% with the amino acid sequence given under SEQ ID NO: 4;
  - c) Nucleic acid molecules, which include the nucleotide sequence shown under Seq ID No. 3 or a complimentary sequence;
  - d) Nucleic acid molecules, the nucleic acid sequence of which has an identity of at least 50% with the nucleic acid sequences described under a) or c);
  - e) Nucleic acid molecules, which hybridise with at least one strand of the nucleic acid molecules described under a) or c) under stringent conditions;
  - f) Nucleic acid molecules, the nucleotide sequence of which deviates from the sequence of the nucleic acid molecules identified under a), b), c), d), e) or f) due to the degeneration of the genetic code; and

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- g) Nucleic acid molecules, which represent fragments, allelic variants and/or derivatives of the nucleic acid molecules identified under a), b), c), d), e) or f).
5. Genetically modified plant cell according to one of Claims 2, 3 or 4, wherein the said foreign nucleic acid molecule is chosen from the group consisting of
- a) DNA molecules, which code at least one antisense RNA, which effects a reduction in the expression of at least one endogenous gene, which codes a Class 3 branching enzyme;
  - b) DNA molecules, which by means of a co-suppression effect lead to the reduction in the expression of at least one endogenous gene, which codes a Class 3 branching enzyme;
  - c) DNA molecules, which code at least one ribozyme, which splits specific transcripts of at least one endogenous gene, which codes a Class 3 branching enzyme;
  - d) DNA molecules, which simultaneously code at least one antisense RNA and at least one sense RNA, wherein the said antisense RNA and the said sense RNA form a double-stranded RNA molecule, which effects a reduction in the expression of at least one endogenous gene, which codes a Class 3 branching enzyme (RNAi technology);
  - e) Nucleic acid molecules introduced by means of in vivo mutagenesis, which lead to a mutation or an insertion of a heterologous sequence in at least one endogenous gene coding a Class 3 branching enzyme, wherein the mutation or insertion effects a reduction in the expression of a gene coding a Class 3 branching enzyme or results in the synthesis of inactive Class 3 branching enzymes;
  - f) Nucleic acid molecules, which code an antibody, wherein the antibody results in a reduction in the activity of a Class 3 branching enzyme due to the bonding to a Class 3 branching enzyme.
  - g) DNA molecules, which contain transposons, wherein the integration of these transposons leads to a mutation or an insertion in at least one endogenous

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gene coding a Class 3 branching enzyme, which effects a reduction in the expression of at least one gene coding a Class 3 branching enzyme, or results in the synthesis of inactive Class 3 branching enzymes; and/or

- h) T-DNA molecules, which, due to insertion in at least one endogenous gene coding a Class 3 branching enzyme, effect a reduction in the expression of at least one gene coding a Class 3 branching enzyme, or result in the synthesis of inactive Class 3 branching enzyme.

6. Plant cell according to one of Claims 1 to 5, which synthesises a modified starch in comparison with corresponding wild type plant cells that have not been genetically modified.
7. Plant containing plant cells according to one of Claims 1 to 6.
8. Plant according to Claim 7, which is a starch-storing plant.
9. Plant according to Claim 8, which is a maize, rice, wheat, rye, oat, barley, cassava, potato, sago, mung bean, pea or sorghum plant.
10. Plant according to Claim 8, which is a potato plant.
11. Propagation material of plants according to one of Claims 7 to 10, containing plant cells according to one of Claims 1 to 6.
12. Harvestable plant parts of plants according to one of Claims 7 to 10, containing plant cells according to one of Claims 1 to 6.
13. Method for the manufacture of a genetically modified plant according to one of Claims 7 to 10, wherein
  - a) a plant cell is genetically modified, whereby the genetic modification leads to the reduction of the activity of a Class 3 vegetable branching enzyme in comparison with corresponding wild type plant cells that have not been genetically modified;
  - b) a plant is regenerated from plant cells from Step a); and

- c) if necessary, further plants are produced with the help of the plants according to Step b).
14. Method according to Claim 13, wherein the genetic modification consists in the introduction of at least one foreign nucleic acid molecule into the genome of the plant.
15. Method according to Claim 14, wherein the said foreign nucleic acid molecule is chosen from the group consisting of
- a) Nucleic acid molecules, which code a protein with the amino acid sequence given under Seq ID No. 4;
  - b) Nucleic acid molecules, which code a protein, the amino acid sequence of which has an identity of at least 50% with the amino acid sequence given under SEQ ID NO: 4;
  - c) Nucleic acid molecules, which include the nucleotide sequence shown under Seq ID No. 3 or a complimentary sequence;
  - d) Nucleic acid molecules, the nucleic acid sequence of which has an identity of at least 50% with the nucleic acid sequences described under a) or c);
  - e) Nucleic acid molecules, which hybridise with at least one strand of the nucleic acid molecules described under a) or c) under stringent conditions;
  - f) Nucleic acid molecules, the nucleotide sequence of which deviates from the sequence of the nucleic acid molecules identified under a), b), c), d), e) or f) due to the degeneration of the genetic code; and
  - g) Nucleic acid molecules, which represent fragments, allelic variants and/or derivatives of the nucleic acid molecules identified under a), b), c), d), e) or f).
16. Method according to Claim 14, wherein the said foreign nucleic acid molecule is chosen from the group consisting of

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- a) DNA molecules, which code at least one antisense RNA, which effects a reduction in the expression of at least one endogenous gene, which codes a Class 3 branching enzyme;
- b) DNA molecules, which by means of a co-suppression effect lead to the reduction in the expression of at least one endogenous gene, which codes a Class 3 branching enzyme;
- c) DNA molecules, which code at least one ribozyme, which splits specific transcripts of at least one endogenous gene, which codes a Class 3 branching enzyme;
- d) DNA molecules, which simultaneously code at least one antisense RNA and at least one sense RNA, wherein the said antisense RNA and the said sense RNA form a double-stranded RNA molecule, which effects a reduction in the expression of at least one endogenous gene, which codes a Class 3 branching enzyme (RNAi technology);
- e) Nucleic acid molecules introduced by means of in vivo mutagenesis, which lead to a mutation or an insertion of a heterologous sequence in at least one endogenous gene coding a Class 3 branching enzyme, wherein the mutation or insertion effects a reduction in the expression of a gene coding a Class 3 branching enzyme or results in the synthesis of inactive Class 3 branching enzymes;
- f) Nucleic acid molecules, which code an antibody, wherein the antibody results in a reduction in the activity of a Class 3 branching enzyme due to the bonding to a Class 3 branching enzyme.
- g) DNA molecules, which contain transposons, wherein the integration of these transposons leads to a mutation or an insertion in at least one endogenous gene coding a Class 3 branching enzyme, which effects a reduction in the expression of at least one gene coding a Class 3 branching enzyme, or results in the synthesis of inactive Class 3 branching enzymes; and/or

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- h) T-DNA molecules, which, due to insertion in at least one endogenous gene coding a Class 3 branching enzyme, effect a reduction in the expression of at least one gene coding a Class 3 branching enzyme, or result in the synthesis of inactive Class 3 branching enzyme.
17. Method according to one of Claims 13 to 17 [sic], wherein the genetically modified plant synthesises a modified starch in comparison with corresponding wild type plants that have not been genetically modified.
18. Nucleic acid molecule, coding for a protein with the enzymatic activity of a Class 3 branching enzyme, chosen from the group consisting of
- a) Nucleic acid molecules, which code a protein with the amino acid sequence given under Seq ID No. 4;
  - b) Nucleic acid molecules, which code a protein, the amino acid sequence of which has an identity of at least 70% with the amino acid sequence given under SEQ ID NO: 4;
  - c) Nucleic acid molecules, which include the nucleotide sequence shown under Seq ID No. 3 or a complimentary sequence;
  - d) Nucleic acid molecules, which have an identity of at least 70% with the nucleic acid sequences described under a) or c);
  - e) Nucleic acid molecules, which hybridise with at least one strand of the nucleic acid molecules described under a) or c) under stringent conditions;
  - f) Nucleic acid molecules, the nucleotide sequence of which deviates from the sequence of the nucleic acid molecules identified under a), b), c), d), e) or f) due to the degeneration of the genetic code; and
  - g) Nucleic acid molecules, which represent fragments, allelic variants and/or derivatives of the nucleic acid molecules identified under a), b), c), d), e) or f).
19. Nucleic acid molecule according to Claim 18, characterised in that it codes a Class 3 branching enzyme of potato.

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20. Vector containing a nucleic acid molecule according to one of Claims 18 or 19.
21. Vector according to Claim 20, wherein the nucleic acid molecule is linked with regulatory sequences, which guarantee transcription into prokaryotic or eukaryotic cells.
22. Vector containing a foreign nucleic acid molecule defined as in Claim 5 under a), b), c) or d).
23. Host cell, which is genetically modified with a nucleic acid molecule according to one of Claims 18 or 19 or with a vector according to one of Claims 20, 21 or 22.
24. Protein with the enzymatic activity of a Class 3 branching enzyme, chosen from the group consisting of
  - a) Proteins, which include the amino acid sequence specified under SEQ ID No. 4, or
  - b) Proteins, which have an identity of at least 70% with the amino acid sequence of the proteins identified under a).
25. Protein according to Claim 24, wherein the Class 3 branching enzyme comes from a potato plant.
26. Modified starch obtainable from a genetically modified plant according to one of Claims 7 to 10, from propagation material according to Claim 11, or from harvestable plant parts according to Claim 12.
27. Method for the manufacture of a modified starch including the step of extracting the starch from a plant cell according to one of Claims 1 to 6.
28. Method for the manufacture of a modified starch including the step of extracting the starch from a plant according to one of Claims 7 to 10, and/or from starch-storing parts of such a plant.
29. Method for the manufacture of a modified starch including the step of extracting the starch from harvestable plant parts according to Claim 12.

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30. Method for the manufacture of a derived starch, wherein modified starch according to Claim 26 or obtainable by means of a method according to one of Claims 27, 28 or 29 is derived.
31. Use of genetically modified plants according to one of Claims 7 to 10 for the manufacture of a modified starch.
32. Modified starch obtainable by means of a method according to one of Claims 27, 28 or 29.
33. Derived starch obtainable by means of a method according to Claim 30.
34. Use of modified starch according to one of Claims 26 or 32 for the manufacture of derived starch.